

1 CGCGTGCAGGTGGCAGTCCTCCCAAAGTACTTGTGTCCGGGTGGT  
 46 GGACTGGATTTCGCTGCGGAGCCCTGGAAGCTGCCTTTCCTTCTCC  
 91 CTGTGCTTAACCAGAGGTGCCCATGGGTGGACAATGAGGCTGGT  
 MetGlyTrpThrMetArgLeuVa  
 136 CACAGCAGCACTGTTACTGGGTCTCATGATGGTGGTCACTGGAGA  
 lThrAlaAlaLeuLeuLeuGlyLeuMetMetValValThrGlyAs  
 181 CGAGGATGAGAACAGCCCGTGTGCCCATGAGGCCCTCTTGACGA  
 pGluAspGluAsnSerProCysAlaHisGluAlaLeuLeuAspGl  
 226 GGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTT  
 uAspThrLeuPheCysGlnGlyLeuGluValPheTyrProGluLe  
 271 GGGGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACTACAG  
 uGlyAsnIleGlyCysLysValValProAspCysAsnAsnTyrAr  
 316 ACAGAAGATCACCTCCTGGATGGAGCCGATAGTCAAGTTCCCGG  
 gGlnLysIleThrSerTrpMetGluProIleValLysPheProGl  
 361 GGCCGTGGACGGCGCAACCTATATCCTGGTGATGGTGGATCCAGA  
 yAlaValAspGlyAlaThrTyrIleLeuValMetValAspProAs  
 406 TGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTG  
 pAlaProSerArgAlaGluProArgGlnArgPheTrpArgHisTr  
 451 GCTGGTAACAGATATCAAGGGCGCCGACCTGAAGGAAGGGAAGAT  
 pLeuValThrAspIleLysGlyAlaAspLeuLysGluGlyLysIl  
 496 TCAGGGCCAGGAGTTATCAGCCTACCAGGCTCCCTCCCCACCGGC  
 eGlnGlyGlnGluLeuSerAlaTyrGlnAlaProSerProProAl  
 541 ACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCAGGA  
 aHisSerGlyPheHisArgTyrGlnPhePheValTyrLeuGlnGl  
 586 AGGAAAAGTCATCTCTCTCTTCCCAAGGAAAACAAAACCTCGAGG  
 uGlyLysValIleSerLeuLeuProLysGluAsnLysThrArgGl  
 631 CTCTTGGAATGGACAGATTTCTGAACCGTTTCCACCTGGGCGA  
 ySerTrpLysMetAspArgPheLeuAsnArgPheHisLeuGlyGl  
 676 ACCTGAAGCAAGCACCCAGTTCATGACCCAGAACTACCAGGACTC  
 uProGluAlaSerThrGlnPheMetThrGlnAsnTyrGlnAspSe  
 721 ACCAACCCTCCAGGCTCCCAGAGAAAGGGCCAGCGAGCCCAAGCA  
 rProThrLeuGlnAlaProArgGluArgAlaSerGluProLysHi  
 766 CAAAAACCAGGCGGAGATAGCTGCCTGCTAGATAGCCGGCTTTGC  
 sLysAsnGlnAlaGluIleAlaAlaCys  
 811 CATCCGGGCATGTGGCCACACTGCCCACCACCGACGATGTGGGTA  
 856 TGGAAACCCCTCTGGATACAGAACCCCTTCTTTTCCAAATTAAAA  
 901 AAAAAAATCATCCAGGAAAAAAAAAAAAAAAAAAAA

Fig. 1

1 GGAGGTGGGGTGAGACAGGACCAGCCCCCTAAGCCTGGTCAGGCCT  
 46 GATCAAGTGCTGTGGCAGTCATGGTGCGAACGCGGTGGCAGCCTC  
     MetValArgThrArgTrpGlnProH  
 91 ACCCTCCGCCGCCCTGCTTCTCCTGGTGCTCGTGTGGCTCCCCC  
     isProProProProLeuLeuLeuLeuValLeuValTrpLeuProG  
 136 AAAGCCTGAGTCTAGACCTGATTGCCTACGTGCCGCAGATAACAG  
     lnSerLeuSerLeuAspLeuIleAlaTyrValProGlnIleThrA  
 181 CCTGGGACCTGGAAGGGAAGATCACAGCCACTACATTCTCTCTGG  
     laTrpAspLeuGluGlyLysIleThrAlaThrThrPheSerLeuG  
 226 AGCAGCCTCGGTGCGTCTTTGATGAGCATGTCTCAACTAAGGACA  
     luGlnProArgCysValPheAspGluHisValSerThrLysAspT  
 271 CCATCTGGCTAGTGGTGGCTTTCAGCAATGCCTCCAGGGACTTTC  
     hrIleTrpLeuValValAlaPheSerAsnAlaSerArgAspPheG  
 316 AGAACCCACAGACTGCTGCTAAGATCCCGACCTTCCCACAGCTGC  
     lnAsnProGlnThrAlaAlaLysIleProThrPheProGlnLeuL  
 361 TGA CTGACGGCCACTATATGACATTACCCCTGTCCCTGGATCAGC  
     euThrAspGlyHisTyrMetThrLeuProLeuSerLeuAspGlnL  
 406 TGCCATGTGAGGACCTGACCGGTGGCAGTGGAGGTGTCCCGTGC  
     euProCysGluAspLeuThrGlyGlySerGlyGlyValProValL  
 451 TTCGGGTGGGCAATGATTTTGGCTGTTACCAGCGACCCTATTGCA  
     euArgValGlyAsnAspPheGlyCysTyrGlnArgProTyrCysA  
 496 ACGCCCCCTCCCCAGCCAGGGCCCTTACAGTGTGAAGTTCCTTG  
     snAlaProLeuProSerGlnGlyProTyrSerValLysPheLeuV  
 541 TAATGGATGCCGCCGGCCACCCAAGGCTGAGACGAAGTGGTCCA  
     alMetAspAlaAlaGlyProProLysAlaGluThrLysTrpSerA  
 586 ACCCCATTTATCTCCACCAAGGAAAGAATCCCAACTCCATTGACA  
     snProIleTyrLeuHisGlnGlyLysAsnProAsnSerIleAspT  
 631 CATGGCCTGGCCGACGGAGCGGCTGTATGATCGTCATAACTTCCA  
     hrTrpProGlyArgArgSerGlyCysMetIleValIleThrSerI  
 676 TCCTCTCTGCCCTGGCCGGCCTCTTGCTCCTGGCTTTCCTGGCAG  
     leLeuSerAlaLeuAlaGlyLeuLeuLeuLeuAlaPheLeuAlaA  
 721 CTTCCACTACGCGT  
     laSerThrThrArg

Fig. 2

**Fig. 3**

946 AAAACAGAGAGCAATACCAAGTGGTCATCCAGGCCAAAGACATGG  
 luAsnArgGluGlnTyrGlnValValIleGlnAlaLysAspMetG  
 991 GCGGCCAGATGGGAGGCTTATCGGGACAACCACTGTGAACATCA  
 lyGlyGlnMetGlyGlyLeuSerGlyThrThrThrValAsnIleT  
 1036 CGCTGACAGATGTCAATGACAACCCACCACGTTTCCCCCAGAACA  
 hrLeuThrAspValAsnAspAsnProProArgPheProGlnAsnT  
 1081 CTATTCATCTTCGAGTTCTTGAATCCTCCCCAGTTGGCACAGCCA  
 hrIleHisLeuArgValLeuGluSerSerProValGlyThrAlaI  
 1126 TTGGAAGTGTCAAAGCAACTGATGCTGACACTGGGAAAAATGCTG  
 leGlySerValLysAlaThrAspAlaAspThrGlyLysAsnAlaG  
 1171 AAGTAGAATACCGAATTATTGATGGTGACGGTACTGATATGTTTG  
 luValGluTyrArgIleIleAspGlyAspGlyThrAspMetPheA  
 1216 ACATCGTGACTGAGAAGGACACACAGGAAGGCATCATCACTGTGA  
 spIleValThrGluLysAspThrGlnGluGlyIleIleThrValL  
 1261 AAAAGCCACTCGACTATGAAAGCCGAAGACTTTTATACTCTGAAAG  
 ysLysProLeuAspTyrGluSerArgArgLeuTyrThrLeuLysV  
 1306 TCGAAGCAGAAAACACCCATGTAGATCCCCGTTTTTTATTACCTAG  
 alGluAlaGluAsnThrHisValAspProArgPheTyrTyrLeuG  
 1351 GACCATTTAAAGATACTACCATAGTGAAAATCTCTATAGAAGATG  
 lyProPheLysAspThrThrIleValLysIleSerIleGluAspV  
 1396 TGGATGAACCTCCTGTTTTTAGTAGGTCCTCCTATCTGTTTGAAG  
 alAspGluProProValPheSerArgSerSerTyrLeuPheGluV  
 1441 TTCATGAAGATATTGAAGTGGGCACAATCATTGGTACTGTAATGG  
 alHisGluAspIleGluValGlyThrIleIleGlyThrValMetA  
 1486 CAAGGGACCCAGATTCTATTTCCAGCCCCATTAGATTTTCCTTGG  
 laArgAspProAspSerIleSerSerProIleArgPheSerLeuA  
 1531 ATCGCCATACTGACCTTGACAGAATCTTTAACATTTCATTCAGGAA  
 spArgHisThrAspLeuAspArgIlePheAsnIleHisSerGlyA  
 1576 ATGGATCTCTTTATACATCAAAACCTCTTGACCGTGAACATCTC  
 snGlySerLeuTyrThrSerLysProLeuAspArgGluLeuSerG  
 1621 AGTGGCATAAATTCGTTAGTTATTGCTGCTGAAATCAACAATCCCA  
 lnTrpHisAsnSerLeuValIleAlaAlaGluIleAsnAsnProL  
 1666 AAGAGACAACACGCGTGGCTGTTTTGTGAGAATTTTGGATGTTA  
 ysGluThrThrArgValAlaValPheValArgIleLeuAspValA  
 1711 ATGACAATGCCCCACAGTTTGCTGTGTTCTATGACACTTTTGTAT  
 snAspAsnAlaProGlnPheAlaValPheTyrAspThrPheValC  
 1756 GTGAAAATGCCAGACCAGGGCAGCTAATACAGACTATAAGTGCAG  
 ysGluAsnAlaArgProGlyGlnLeuIleGlnThrIleSerAlaV

Fig. 3 Continued

1801 TAGACAAAGATGACCCCTTAGGTGGACAGAAATTTTTTTCAGTT  
 alAspLysAspAspProLeuGlyGlyGlnLysPhePhePheSerL  
 1846 TAGCTGCTGTCAATCCAACTTCACAGTACAGGATAATGAAGATA  
 euAlaAlaValAsnProAsnPheThrValGlnAspAsnGluAspA  
 1891 ATACTGCCAGAATCTTAACCAGAAAAAATGGATTCAATAGACATG  
 snThrAlaArgIleLeuThrArgLysAsnGlyPheAsnArgHisG  
 1936 AAATCAGTACCTATCTCTTGCCTGTGGTGATATCAGACAATGATT  
 luIleSerThrTyrLeuLeuProValValIleSerAspAsnAspT  
 1981 ACCCGATTGAGAGCAGCACAGGCACACTGACCATTGAGTGTGTG  
 yrProIleGlnSerSerThrGlyThrLeuThrIleArgValCysA  
 2026 CTTGTGACAGCCAAGGCAACATGCAATCCTGCAGTGCTGAAGCCC  
 laCysAspSerGlnGlyAsnMetGlnSerCysSerAlaGluAlaL  
 2071 TGCTCCTCCCTGCCGGCCTCAGCACTGGGGCCTTGATCGCCATCC  
 euLeuLeuProAlaGlyLeuSerThrGlyAlaLeuIleAlaIleL  
 2116 TCCTCTGCATCATCATTCTACTGGTTATAGTAGTACTGTTTGCAG  
 euLeuCysIleIleIleLeuLeuValIleValValLeuPheAlaA  
 2161 CTCTGAAAGGACAGCGAAAAAAGAGCCTCTGATCTTGTCAAAAG  
 laLeuLysGlyGlnArgLysLysGluProLeuIleLeuSerLysG  
 2206 AAGATATCAGAGACAACATTGTGAGCTATAACGATGAGGGTGGTG  
 luAspIleArgAspAsnIleValSerTyrAsnAspGluGlyGlyG  
 2251 GAGAGGAGGACACCCAGGCCTTTGATATCGGCACCCTGAGGAATC  
 lyGluGluAspThrGlnAlaPheAspIleGlyThrLeuArgAsnP  
 2296 CTGCAGCCATTGAGGAAAAAAGCTCCGGCGAGATATTATTCCAG  
 roAlaAlaIleGluGluLysLysLeuArgArgAspIleIleProG  
 2341 AAACGTTATTTATTCCTCGGAGGACTCCTACAGCTCCAGATAACA  
 luThrLeuPheIleProArgArgThrProThrAlaProAspAsnT  
 2386 CGGACGTCCGGGATTTTCATTAATGAAAGGCTAAAAGAGCATGATC  
 hrAspValArgAspPheIleAsnGluArgLeuLysGluHisAspL  
 2431 TTGACCCACCGCACCCCCCTACGACTCACTTGCAACCTATGCCT  
 euAspProThrAlaProProTyrAspSerLeuAlaThrTyrAlaT  
 2476 ATGAAGGAAATGATTCCATTGCTGAATCTCTGAGTTCATTAGAAT  
 yrGluGlyAsnAspSerIleAlaGluSerLeuSerSerLeuGluS  
 2521 CAGGTACTACTGAAGGAGACCAAACTACGATTACCTCCGAGAAT  
 erGlyThrThrGluGlyAspGlnAsnTyrAspTyrLeuArgGluT  
 2566 GGGGCCCTCGGTTTAATAAGCTAGCAGAAATGTATGGTGGTGGGG  
 rpGlyProArgPheAsnLysLeuAlaGluMetTyrGlyGlyGlyG  
 2611 AAAGTGACAAAGACTCTTAACGTAGGATATATGTTCTGTTCAAAC  
 luSerAspLysAspSer  
 2656 AAGAGAAAGTAACTCTACCCATGCTGTCTCCACTTCACAATATTT  
 2701 GATATTCAGGACATTCCTGCAGTCAGCACAAATTTTTTCTCA

Fig. 3 Continued

1 AAGATGGTAGCAAAGTAATGAGTTGAGAGTTGCTTTCAGTGGTGT  
 46 GTTACCGGAGATAGAAAAATGAAGGATACAGGCTAAGGGACCAA  
 91 CTGCAGTGTGATGGAACTGAGTTTTAATGATGCCTCTTAGGAAA  
 136 TGAATTTCCAACATGTAGTACACTATTCATCTTCGAGTTCTTGAAT  
 181 CCTCCCCAGTTGGCACAGCCATTGGAAGTGTCAAAGCAACTGATG  
 226 CTGACACTGGGAAAAATGCTGAAGTAGAATACCGAATTATTGATG  
  
 271 GTGACGGTACTGATATGTTTGACATCGTGACTGAGAAGGACACAC  
     MetPheAspIleValThrGluLysAspThrG  
  
 316 AGGAAGGCATCATCACTGTGAAAAGCCACTCGACTATGAGAGCC  
     InGluGlyIleIleThrValLysLysProLeuAspTyrGluSerA  
  
 361 GAAGACTTTTATACTCTGAAAGTCGAAGCAGAAAACACCCATGTAG  
     rgArgLeuTyrThrLeuLysValGluAlaGluAsnThrHisvalA  
  
 406 ATCCCGTTTTTATTACCTAGGACCATTAAAGATACTACCATAG  
     spProArgPheTyrTyrLeuGlyProPheLysAspThrThrIleV  
  
 451 TGAAAATCTCTATAGAAGATGTGGATGAACCTCCTGTTTTAGTA  
     alLysIleSerIleGluAspValAspGluProProValPheSerA  
  
 496 GGTCTCCTATCTGTTTGAAGTTCATGAAGATATTGAAGTGGGCA  
     rgSerSerTyrLeuPheGluValHisGluAspIleGluValGlyT  
  
 541 CAATCATTTGGTACTGTAATGGCAAGGGACCCAGATTCTATTTCCA  
     hrIleIleGlyThrValMetAlaArgAspProAspSerIleSerS  
  
 586 GCCCCATTAGATTTTCCTTGGATCGCCATACTGACCTTGACAGAA  
     erProIleArgPheSerLeuAspArgHisThrAspLeuAspArgI  
  
 631 TCTTTAACATTTCATTCAGGAAATGGATCTCTTTATACATCAAAAC  
     lePheAsnIleHisSerGlyAsnGlySerLeuTyrThrSerLysP  
  
 676 CTCTTGACCGTGAACCTATCTCAGTGGCATAATTCTGTTAGTTATTG  
     roLeuAspArgGluLeuSerGlnTrpHisAsnSerLeuValIleA  
  
 721 CTGCTGAAATCAACAATCCCAAAGAGACAACACGCGTGGCTGTTT  
     laAlaGluIleAsnAsnProLysGluThrThrArgValAlaValP  
  
 766 TTGTGAGAATTTTGGATGTTAATGACAATGCCCCACAGTTTGCTG  
     heValArgIleLeuAspValAsnAspAsnAlaProGlnPheAlaV  
  
 811 TGTCTATGACACTTTTGTATGTGAAAATGCCAGACCAGGGCAGC  
     alPheTyrAspThrPheValCysGluAsnAlaArgProGlyGlnL  
  
 856 TAATACAGACTATAAGTGCAGTAGACAAAGATGACCCTTTAGGTG  
     euIleGlnThrIleSerAlaValAspLysAspAspProLeuGlyG  
  
 901 GACAGAAATTTTTTTTTCAGTTTAGCTGCTGTCAATCCAACTTCA  
     lyGlnLysPhePhePheSerLeuAlaAlaValAsnProAsnPheT  
  
 946 CAGTACAGGATAATGAAGATAATACTGCCAGAATCTTAACCAGAA  
     hrValGlnAspAsnGluAspAsnThrAlaArgIleLeuThrArgL

Fig. 4

991 AAAATGGATTCAATAGACATGAAATCAGTACCTATCTCTTGCCTG  
 ysAsnGlyPheAsnArgHisGluIleSerThrTyrLeuLeuProV  
 1036 TGGTGATATCAGACAATGATTACCCGATTTCAGAGCAGCACAGGCA  
 alValIleSerAspAsnAspTyrProIleGlnSerSerThrGlyT  
 1081 CACTGACCATTCGAGTGTGTGCTTGTGACAGCCAAGGCAACATGC  
 hrLeuThrIleArgValCysAlaCysAspSerGlnGlyAsnMetG  
 1126 AATCCTGCAGTGTGCTGAAGCCCTGCTCCTCCCTGCCGGCCTCAGCA  
 lnSerCysSerAlaGluAlaLeuLeuLeuProAlaGlyLeuSerT  
 1171 CTGGGGCCCTTGATCGCCATCCTCCTCTGCATCATCATTCTACTGG  
 hrGlyAlaLeuIleAlaIleLeuLeuCysIleIleIleLeuLeuV  
 1216 TTATAGTAGTACTGTTTGCAGCTCTGAAAGGACAGCGAAAAAAG  
 alIleValValLeuPheAlaAlaLeuLysGlyGlnArgLysLysG  
 1261 AGCCTCTGATCTTGTCAAAGAAGATATCAGAGACAACATTGTGA  
 luProLeuIleLeuSerLysGluAspIleArgAspAsnIleValS  
 1306 GCTATAACGATGAGGGTGGTGGAGAGGAGGACACCCAGGCCTTTG  
 erTyrAsnAspGluGlyGlyGlyGluGluAspThrGlnAlaPheA  
 1351 ATATCGGCACCCCTGAGGAATCCTGCAGCCATTGAGGAAAAAAGC  
 spIleGlyThrLeuArgAsnProAlaAlaIleGluGluLysLysL  
 1396 TCCGGCGAGATATTATTCCAGAAACGTTATTTATTCCTCGGAGGA  
 euArgArgAspIleIleProGluThrLeuPheIleProArgArgT  
 1441 CTCCTACAGCTCCAGATAACACGGACGTCCGGGATTTCAATTAATG  
 hrProThrAlaProAspAsnThrAspValArgAspPheIleAsnG  
 1486 AAAGGCTAAAAGAGCATGATCTTGACCCACCGCACCCCCCTACG  
 luArgLeuLysGluHisAspLeuAspProThrAlaProProTyrA  
 1531 ACTCACTTGCAACCTATGCCTATGAAGGAAATGATTCCATTGCTG  
 spSerLeuAlaThrTyrAlaTyrGluGlyAsnAspSerIleAlaG  
 1576 AATCTCTGAGTTCATTAGAATCAGGTACTACTGAAGGAGACCAAA  
 luSerLeuSerSerLeuGluSerGlyThrThrGluGlyAspGlnA  
 1621 ACTACGATTACCTCCGAGAATGGGGCCCTCGGTTTAATAAGCTAG  
 snTyrAspTyrLeuArgGluTrpGlyProArgPheAsnLysLeuA  
 1666 CAGAAATGTATGGTGGTGGGGAAAGTGACAAAGACTCTTAACGTA  
 laGluMetTyrGlyGlyGlyGluSerAspLysAspSer  
 1711 GGATATATGTTCTGTTCAAACAAGAGAAAGTAACTCTACCCATGC  
 1756 TGTCTCCACTTCACAATATTTGATATTCAGGAGCATTTCTCTGCAG  
 1801 TCAGCACAATTTTTTCTCA

Fig. 4 Continued

1 CAAAGGCTGGAGACAAGTGGGTTGGGGTTGGTTTTAATTTGGCA  
 46 GTTGTAATTAATGGTCAATTTTAATAGTCCGTAATTGATGGCAGC  
 91 CTGCTGTGGTACATGTGTGAAAGATTATCACTTTGAATATACGGA  
 136 ATGTGATAGCAGTGGCTCCAGGTGGAGAGTTGCCATTCCAAATTC  
 181 TGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGCAAAGA  
  
 226 ATGCACTCTTCTTGGATCCCTCGTGGAAACTACATAGAATCTAAT  
 MetHisSerSerTrpIleProArgGlyAsnTyrIleGluSerAsn  
  
 271 CGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAG  
 ArgAspAspCysThrValSerLeuIleTyrAlaValHisLeuLys  
  
 316 AAGTCAGGCTATGTCTTCTTTGAGTACCAGTATGTCGACAACAAC  
 LysSerGlyTyrValPhePheGluTyrGlnTyrValAspAsnAsn  
  
 361 ATCTTCTTTGAGTTCTTTATTCAAATGATCAGTGCCAGGAGATG  
 IlePhePheGluPhePheIleGlnAsnAspGlnCysGlnGluMet  
  
 406 GACACCACCACTGACAAGTGGGTAAACTTACAGACAATGGAGAA  
 AspThrThrThrAspLysTrpValLysLeuThrAspAsnGlyGlu  
  
 451 TGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTC  
 TrpGlySerHisSerValMetLeuLysSerGlyThrAsnIleLeu  
  
 496 TACTGGAGAACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAG  
 TyrTrpArgThrThrGlyIleLeuMetGlySerLysAlaValLys  
  
 541 CCTGTGCTGGTAAAAAATATCACAATTGAAGGGGTGGCGTACACA  
 ProValLeuValLysAsnIleThrIleGluGlyValAlaTyrThr  
  
 586 TCAGAAATGTTTTCTTTGCAAGCCAGGCACATTCAGCAACAAACCA  
 SerGluCysPheProCysLysProGlyThrPheSerAsnLysPro  
  
 631 GGTTCATTCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAG  
 GlySerPheAsnCysGlnValCysProArgAsnThrTyrSerGlu  
  
 676 AAAGGAGCCAAAGAATGTATAAGGTGTAAAGACGACTCTCAATTT  
 LysGlyAlaLysGluCysIleArgCysLysAspAspSerGlnPhe  
  
 721 TCAGAGGAAGGATCCAGTGAGTGACAGAGCGCCCTCCCTGTACC  
 SerGluGluGlySerSerGluCysThrGluArgProProCysThr  
  
 766 ACAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA  
 ThrLysAspTyrPheGlnIleHisThrProCysAspGluGluGly  
  
 811 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAAATCTGCCGG  
 LysThrGlnIleMetTyrLysTrpIleGluProLysIleCysArg  
  
 856 GAGGATCTCACAGATGCTATTAGATTGCCCCCTTCTGGAGAGAAG  
 GluAspLeuThrAspAlaIleArgLeuProProSerGlyGluLys  
  
 901 AAGGATTGTCCGCTTGCAACCCTGGATTTTATAACAATGGATCA  
 LysAspCysProProCysAsnProGlyPheTyrAsnAsnGlySer  
  
 946 TCTTCTTGCCATCCCTGTCTCTGGAACATTTTCAGATGGAACC  
 SerSerCysHisProCysProProGlyThrPheSerAspGlyThr

Fig. 5



991 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCAC TTGGC  
LysGluCysArgProCysProAlaGlyThrGluProAlaLeuGly

1036 TTTGAATATAAATGGTGGGAATGTCCTTCCTGGCAACATGAAA ACT  
PheGluTyrLysTrpTrpAsnValLeuProGlyAsnMetLysThr

1081 TCCTGCTTCAATGTTGGGAATTCAAAGTGCGATGGAATGAATGGT  
SerCysPheAsnValGlyAsnSerLysCysAspGlyMetAsnGly

1126 TGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT  
TrpGluValAlaGlyAspHisIleGlnSerGlyAlaGlyGlySer

1171 GACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAA  
AspAsnAspTyrLeuIleLeuAsnLeuHisIleProGlyPheLys

1216 CCACCAACATCTATGACTGGAGCCACGGGTTCTGAACTAGGAAGA  
ProProThrSerMetThrGlyAlaThrGlySerGluLeuGlyArg

1261 ATAACATTTGTC TTTGAGACCCTCTGTT CAGCTGACTGTGTTT TG  
IleThrPheValPheGluThrLeuCysSerAlaAspCysValLeu

1306 TACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA  
TyrPheMetValAspIleAsnArgLysSerThrAsnValValGlu

1351 TCGTGGGGTGGAAACCAAAGAAAAACAAGCTTACACCCATATCATC  
SerTrpGlyGlyThrLysGluLysGlnAlaTyrThrHisIleIle

1396 TTCAAGAATGCAACTTTTACATTTACATGGGGCATTCCCAGAGAA  
PheLysAsnAlaThrPheThrPheThrTrpGlyIleProArgGlu

1441 CTAATTCAGGGTCCAAGATAATAGACGGTTCCNCCATTGACATGT  
LeuIleGlnGlyProArg

1486 TTGAAGGATTTATTCCTATTAC

Fig. 5 Continued

**Fig. 6**

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC  
 SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal  
 946 TGCAAGGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGTGG  
 CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp  
 991 ACCACGTTCTGAAGGCGCGGCTGGCATGCTCTGCCCCGAAGTGG  
 ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp  
 1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC  
 GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp  
 1081 ACCTCCTGGCACAAACACCACCTTCTTTGGGGTTTTTCAAGCACAG  
 ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln  
 1126 TGGGGTGACATGTACCTGTGCGCCATCTGTGAGTACCAGTTGGAA  
 TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu  
 1171 GAGATCCAGCGGGTGTTTGAGGGCCCTATAAGGAGTACCATGAG  
 GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu  
 1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT  
 GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro  
 1261 CGGCCTGGCTCGTGCATTAACAACCTGGCATCGGCGCCACGGCTAC  
 ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr  
 1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG  
 ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys  
 1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC  
 LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg  
 1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC  
 ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla  
 1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC  
 AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe  
 1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG  
 IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly  
 1531 CCCTGGGTTACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG  
 ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu  
 1576 CCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGCTGCTCTTT  
 ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe  
 1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC  
 AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys  
 1666 ATAAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCGGGACCCC  
 IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 6 Continued

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT  
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly

1756 GGCCACTTTGGATCTTTACTGATCCAGCATGTGATGACCTCGGAC  
GlyHisPheGlySerLeuLeuIleGlnHisValMetThrSerAsp

1801 ACTTCAGGCATTTGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCC  
ThrSerGlyIleCysAsnLeuArgGlySerLysLysValArgPro

1846 ACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGCTG  
ThrProLysAsnIleThrValValAlaGlyThrAspLeuValLeu

1891 CCCTGCCACCTCTCCTCCACTTGGCCCCGGGGTTCAGTGGTATTT  
ProCysHisLeuSerSerThrTrpProArgGlySerValValPhe

1936 TAAACTTGCCTTCTTCCTGTACAGGGCTGGGAAAGGCTGTGTTAG  
1981 GGGAAAAAAGGAAAGGGTGGGCCTGCTGTGGACAATGGCATACT  
2026 CTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAAC TTATTG  
2071 TGTCCCCGCGTATTTATTTGTTGTAAATATTTGAGTATTTTTATA  
2116 TTGACAAATAAAATGGAGAAAATGAAAAAAAAAAAAAAAAA

Fig. 6 Continued

Fig. 7

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTG  
 SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal  
 946 TGCAAGGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGTGG  
 CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp  
 991 ACCACGTTTCCTGAAGGCGCGGCTGGCATGCTCTGCCCCGAAGTGG  
 ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp  
 1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC  
 GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp  
 1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG  
 ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln  
 1126 TGGGGTGACATGTACCTGTGCGCCATCTGTGAGTACCAGTTGGAA  
 TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu  
 1171 GAGATCCAGCGGGTGTGTTGAGGGCCCCCTATAAGGAGTACCATGAG  
 GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu  
 1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT  
 GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro  
 1261 CGGCCTGGCTCGTGCATTAACAACCTGGCATCGGCGCCACGGCTAC  
 ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr  
 1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG  
 ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys  
 1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC  
 LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg  
 1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC  
 ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla  
 1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC  
 AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe  
 1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG  
 IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly  
 1531 CCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG  
 ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu  
 1576 CCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGCTGCTCTTT  
 ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe  
 1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC  
 AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys  
 1666 ATAAAGTATCGCTCCTGTGCAGACTGTGTCTCGCCCGGGACCCC  
 IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 7 Continued

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT  
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly

1756 GGCCACTTTGGATCTTTACTGATCCAGCATGTGATGACCTCGGAC  
GlyHisPheGlySerLeuLeuIleGlnHisValMetThrSerAsp

1801 ACTTCAGGCATTTGCAACCTCCGTGGCAGTAAGATACAGTCAGGC  
ThrSerGlyIleCysAsnLeuArgGlySerLysIleGlnSerGly

1846 CCACTNCCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTG  
ProLeuProLysAsnIleThrValValAlaGlyThrAspLeuVal

1891 CTGCCCTGCCACCTCTCCTCCAACCTGGCCCTGCCCCGACTCCAAC  
LeuProCysHisLeuSerSerAsnLeuAlaLeuProAspSerAsn

1936 CCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGG  
ProGluGluSerSerVal

1981 ANAGCGTGGGAGGTGTAGCTCCTACTTTTGCACAGGCACCAGCTA  
2026 TCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGGGACAGATAC  
2071 TGCCCAGCACCCACCCGGCCATGAGGACCTGCTCTGCTCAGCACG  
2116 GGCAC TGCACTTGGTGTGGTCACCAGGGCACCAGCTCGCAGAAGG  
2161 CATCTTCCTCCTCTCTGTGAATCACAGACACGCGGGACCCAGCC  
2206 GCCAAAATTTTCAAGGCAGAAGTTNAAGATGTGTGTTTGNTGTAT  
2251 TTGACATGTGTTTGTGTGTGTGTGTATGTGTGTG

Fig. 7 Continued

Fig. 8



856 GTCACTAATGGCTATGATAAAGATGGCTTTGTTTCAGGATATACAG  
 ValThrAsnGlyTyrAspLysAspGlyPheValGlnAspIleGln  
 901 AATGACATTCATGCCAGTTCTTCCCTGAATGGCAGAAGCACTGAA  
 AsnAspIleHisAlaSerSerSerLeuAsnGlyArgSerThrGlu  
 946 GAAGTAAAGCCCATTGATGAAAACCTGGGGCAAACCTGGAAAATCT  
 GluValLysProIleAspGluAsnLeuGlyGlnThrGlyLysSer  
 991 GCTGTTTGCATTACCAAGATATAAATGATGATCATGTTGAAGAT  
 AlaValCysIleHisGlnAspIleAsnAspAspHisValGluAsp  
 1036 GTTACAGGAATTCAGCATTTGACAAGCGATTGAGACAGTGAAGTT  
 ValThrGlyIleGlnHisLeuThrSerAspSerAspSerGluVal  
 1081 TACTGTGATTCTATGGAACAATTTGGACAAGAAGAGTCTTTAGAC  
 TyrCysAspSerMetGluGlnPheGlyGlnGluGluSerLeuAsp  
 1126 AGCTTTACGTCCAACAATGGACCATTTCAGTATTACTTGGGTGGT  
 SerPheThrSerAsnAsnGlyProPheGlnTyrTyrLeuGlyGly  
 1171 CATTCCAGTCAACCCATGGAAAATTCTGGATTTCTGTAAGATATT  
 HisSerSerGlnProMetGluAsnSerGlyPheArgGluAspIle  
 1216 CAAGTACCTCCTGGAAATGGCAACATTGGGAATATGCAGGTGGTT  
 GlnValProProGlyAsnGlyAsnIleGlyAsnMetGlnValVal  
 1261 GCAGTTGAAGGAAAAGGTGAAGTCAAGCATGGAGGAGAAGATGGC  
 AlaValGluGlyLysGlyGluValLysHisGlyGlyGluAspGly  
 1306 AGGAATAACAGCGGAGCACACACCGGGAGAAGCGAGGCGGAGAA  
 ArgAsnAsnSerGlyAlaProHisArgGluLysArgGlyGlyGlu  
 1351 ACTGACGAATTCTCTAATGTTAGAAGAGGAAGAGGACATAGGATG  
 ThrAspGluPheSerAsnValArgArgGlyArgGlyHisArgMet  
 1396 CAACACTTGAGCGAAGGAACCAAGGGCCGGCAGGTGGGAAGTGGGA  
 GlnHisLeuSerGluGlyThrLysGlyArgGlnValGlySerGly  
 1441 GGTGATGGGGAGCGCTGGGGCTCCGACAGAGGGTCCCGAGGCAGC  
 GlyAspGlyGluArgTrpGlySerAspArgGlySerArgGlySer  
 1486 CTAATGAGCAGATCGCCCTCGTGCTGATGAGACTGCAGGAGGAC  
 LeuAsnGluGlnIleAlaLeuValLeuMetArgLeuGlnGluAsp  
 1531 ATGCAGAATGTCCTTCAGAGACTGCAGAACTGGAAATGCTGACT  
 MetGlnAsnValLeuGlnArgLeuGlnLysLeuGluMetLeuThr  
 1576 GCTTTGCAGGCAAAATCATCAACATCAACATTGCAGACTGCTCCT  
 AlaLeuGlnAlaLysSerSerThrSerThrLeuGlnThrAlaPro  
 1621 CAGCCCACCTCACAGAGACCATCTTGGTGGCCCTTCGAGATGTCT  
 GlnProThrSerGlnArgProSerTrpTrpProPheGluMetSer

Fig. 8 Continued

1666 CCTGGTGTGCTAACGTTTGCCATCATATGGCCTTTTATTGCACAG  
ProGlyValLeuThrPheAlaIleIleTrpProPheIleAlaGln

1711 TGGTTGGTGTATTTATACTATCAAAGAAGGAGAAGAAACTGAAC  
TrpLeuValTyrLeuTyrTyrGlnArgArgArgArgLysLeuAsn

1756 TGAGGGAAAATGGTGTTTTCTCAAGAAGACTACTGGAAGTGGAT  
1801 GACCTCAGAATGAACTGGATTGTGGTGTTCACAAGAAAATCTTAG  
1849 TTTGTGATGATTACATTGCTTTTTGTTGTCCNGTAGTTTAGTTTG  
1891 TGTACATATATACACATATATATTTTGCCTACACAAACG

Fig. 8 Continued

1000000 0500000 1000000 1000000

Fig. 9

Fig. 10

991 TACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGA  
 sThrThrLysAspTyrPheGlnIleHisThrProCysAspGluG1  
 1036 AGGAAAGACACAGATAATGTACAAGTGGATAGAGCCCAAAATCTG  
 uGlyLysThrGlnIleMetTyrLysTrpIleGluProLysIleCy  
 1081 CCGGGAGGATCTCACAGATGCTATTAGATTGCCCCCTTCTGGAGA  
 sArgGluAspLeuThrAspAlaIleArgLeuProProSerGlyG1  
 1126 GAAGAAGGATTGTCCGCCTTGCAACCCTGGATTTTATAACAATGG  
 uLysLysAspCysProProCysAsnProGlyPheTyrAsnAsnG1  
 1171 ATCATCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTCAGATGG  
 ySerSerSerCysHisProCysProProGlyThrPheSerAspG1  
 1216 AACCAAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACT  
 yThrLysGluCysArgProCysProAlaGlyThrGluProAlaLe  
 1261 TGGCTTTGAATATAAAATGGTGAATGTCCTTCCTGGCAACATGAA  
 uGlyPheGluTyrLysTrpTrpAsnValLeuProGlyAsnMetLy  
 1306 AACTTCCTGCTTCAATGTTGGGAATTCAAAGTGGCATGGAATGAA  
 sThrSerCysPheAsnValGlyAsnSerLysCysAspGlyMetAs  
 1351 TGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGG  
 nGlyTrpGluValAlaGlyAspHisIleGlnSerGlyAlaGlyG1  
 1396 TTCTGACAATGATTACCTGATCTTAAACTTGCATATCCCAGGATT  
 ySerAspAsnAspTyrLeuIleLeuAsnLeuHisIleProGlyPh  
 1441 TAAACCACCAACATCTATGACTGGAGCCACGGGTCTGAACTAGG  
 eLysProProThrSerMetThrGlyAlaThrGlySerGluLeuG1  
 1486 AAGAATAACATTTGTCTTTGAGACCCTCTGTTTCAGCTGACTGTGT  
 yArgIleThrPheValPheGluThrLeuCysSerAlaAspCysVa  
 1531 TTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGT  
 lLeuTyrPheMetValAspIleAsnArgLysSerThrAsnValVa  
 1576 AGAATCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATAT  
 lGluSerTrpGlyGlyThrLysGluLysGlnAlaTyrThrHisIl  
 1621 CATCTTCAAGAATGCAACTTTTACATTTACATGGGGCATTTCCAG  
 eIlePheLysAsnAlaThrPheThrPheThrTrpGlyIleProAr  
 1666 AGAACTAATTCAGGGTCCAAGATAATAGACGGTTCCNCCATTGAC  
 gGluLeuIleGlnGlyProArg  
 1711 ATGTTTGAAGGATTATTTCCTATTAC

Fig. 10 Continued

Fig. 11

901 TCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTC  
 SerAspCysTyrAlaGluGlnValValAlaArgValAlaArgVal  
 946 TGCAAGGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGTGG  
 CysLysGlyAspMetGlyGlyAlaArgThrLeuGlnArgLysTrp  
 991 ACCACGTTCTTGAAGGCGGGCTGGCATGCTCTGCCCCGAACTGG  
 ThrThrPheLeuLysAlaArgLeuAlaCysSerAlaProAsnTrp  
 1036 CAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGAC  
 GlnLeuTyrPheAsnGlnLeuGlnAlaMetHisThrLeuGlnAsp  
 1081 ACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAG  
 ThrSerTrpHisAsnThrThrPhePheGlyValPheGlnAlaGln  
 1126 TGGGGTGACATGTACCTGTCGGCCATCTGTGAGTACCAGTTGGAA  
 TrpGlyAspMetTyrLeuSerAlaIleCysGluTyrGlnLeuGlu  
 1171 GAGATCCAGCGGGTGTGTTGAGGGCCCCCTATAAGGAGTACCATGAG  
 GluIleGlnArgValPheGluGlyProTyrLysGluTyrHisGlu  
 1216 GAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCT  
 GluAlaGlnLysTrpAspArgTyrThrAspProValProSerPro  
 1261 CGGCCTGGCTCGTGCATTAACAACCTGGCATCGGCGCCACGGCTAC  
 ArgProGlySerCysIleAsnAsnTrpHisArgArgHisGlyTyr  
 1306 ACCAGCTCCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAG  
 ThrSerSerLeuGluLeuProAspAsnIleLeuAsnPheValLys  
 1351 AAGCACCCGCTGATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGC  
 LysHisProLeuMetGluGluGlnValGlyProArgTrpSerArg  
 1396 CCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGGCC  
 ProLeuLeuValLysLysGlyThrAsnPheThrHisLeuValAla  
 1441 GACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTC  
 AspArgValThrGlyLeuAspGlyAlaThrTyrThrValLeuPhe  
 1486 ATTGGCACAGGAGACGGCTGGCTGCTCAAGGCTGTGAGCCTGGGG  
 IleGlyThrGlyAspGlyTrpLeuLeuLysAlaValSerLeuGly  
 1531 CCCTGGGTTACACTGATTGAGGAGCTGCAGCTGTTTGACCAGGAG  
 ProTrpValHisLeuIleGluGluLeuGlnLeuPheAspGlnGlu  
 1576 CCCATGAGAAGCCTGGTGTCTATCTCAGAGCAAAAAGCTGCTCTTT  
 ProMetArgSerLeuValLeuSerGlnSerLysLysLeuLeuPhe  
 1621 GCCGGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGACTGC  
 AlaGlySerArgSerGlnLeuValGlnLeuProValAlaAspCys  
 1666 ATTAAGTATCGCTCCTGTGCAGACTGTGTCCTCGCCCCGGGACCCC  
 IleLysTyrArgSerCysAlaAspCysValLeuAlaArgAspPro

Fig. 11 Continued

1711 TATTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGT  
TyrCysAlaTrpSerValAsnThrSerArgCysValAlaValGly

1756 GGCCACTCTGGATCTCTACTGATCCAGCATGTGATGACCTCGGAC  
GlyHisSerGlySerLeuLeuIleGlnHisValMetThrSerAsp

1801 ACTTCAGGCATCTGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCC  
ThrSerGlyIleCysAsnLeuArgGlySerLysLysValArgPro

1846 ACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGCTG  
ThrProLysAsnIleThrValValAlaGlyThrAspLeuValLeu

1891 CCCTGCCACCTCTCCTCCACTTGGCCCCGGGGTTCAGTGGTATTT  
ProCysHisLeuSerSerThrTrpProArgGlySerValValPhe

1936 TATACTTGCCTTCTTCTGTACAGGGCTGGGAAAGGCTGTGTGAG  
TyrThrCysLeuLeuProValGlnGlyTrpGluArgLeuCysGlu

1981 GGGAAAAAAGGAAAGGGTGGGCCTGCTGTGGACAATGGCATACT  
GlyLysLysArgLysGlyTrpAlaCysCysGlyGlnTrpHisThr

2026 CTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAAC TTATTG  
LeuPheGlnPro

2071 TGTCCCCGCGTATTTATTTGTTGTAAATATTTGAGTATTTTTATA  
2116 TTGACAAATAAAATGGAGAAAATGAAAAAAAAAAAAAAAAAAAA

Fig. 11 Continued



1 CGCTCCATGTATNAGTTTCATGCAGGCTCTTGGGAAAGCTGGTGC  
 MetTyr---PheHisAlaGlySerTrpGluSerTrpCys  
 46 TGCTGCTGCCTGATTCCCGCCGACAGACCTTGGGACCGGGGCCAA  
 CysCysCysLeuIleProAlaAspArgProTrpAspArgGlyGln  
 91 CACTGGCAGCTGGAGATGGCGGACACGAGATCCGTGCACGAGACT  
 HisTrpGlnLeuGluMetAlaAspThrArgSerValHisGluThr  
 136 AGGTTTGAGGCGGCCGTGAAGGTGATCCAGAGTTTGCCGAAGAAT  
 ArgPheGluAlaAlaValLysValIleGlnSerLeuProLysAsn  
 181 GATTCATTCCAGCCAACAAATGAAATGATGCTTAAATTTTATAGC  
 AspSerPheGlnProThrAsnGluMetMetLeuLysPheTyrSer  
 226 TTCTATAAGCAGGCAACTGAAGGACCCTGTAACTTTCAAGGCCT  
 PheTyrLysGlnAlaThrGluGlyProCysLysLeuSerArgPro  
 271 GGATTTTGGGATCCTATTGGAAGATATAAATGGGATGCTTGGAGT  
 GlyPheTrpAspProIleGlyArgTyrLysTrpAspAlaTrpSer  
 316 TCACTGGGTGATATGACCAAAGAGGAAGCCATGATTGCATATGTT  
 SerLeuGlyAspMetThrLysGluGluAlaMetIleAlaTyrVal  
 361 GAAGAAATGAAAAAGATTATTGAACTATGCCAATGACTGAGAAA  
 GluGluMetLysLysIleIleGluThrMetProMetThrGluLys  
 406 GTTGAAGAATTGCTGCGTGTCATAGGTCCATTTTATGAAATTGTC  
 ValGluGluLeuLeuArgValIleGlyProPheTyrGluIleVal  
 451 GAGGACAAAAAGAGTGGCAGGAGTTCTGATATAACCTCAGTCCGA  
 GluAspLysLysSerGlyArgSerSerAspIleThrSerValArg  
 496 CTGGAGAAAATCTCTAAATGTTTAGAAGATCTTGGTAATGTTCTC  
 LeuGluLysIleSerLysCysLeuGluAspLeuGlyAsnValLeu  
 541 ACTTCTACTCCAAACGCCAAAACCGTTAATGGTAAAGCTGAAAGC  
 ThrSerThrProAsnAlaLysThrValAsnGlyLysAlaGluSer  
 586 AGTGACAGTGGAGCCGAGTCTGAGGAAGAAGAGGCCCAAGAAGAA  
 SerAspSerGlyAlaGluSerGluGluGluGluAlaGlnGluGlu  
 631 GTGAAAGGAGCAGAACAAAGTGATAATGATAAGAAAATGATGAAG  
 ValLysGlyAlaGluGlnSerAspAsnAspLysLysMetMetLys  
 676 AAGTCAGCAGACCATAAGAATTTGGAAGTCATTGTCACTAATGGC  
 LysSerAlaAspHisLysAsnLeuGluValIleValThrAsnGly  
 721 TATGATAAAGATGGCTTTGTTCAGGATATACAGAATGACATTCAT  
 TyrAspLysAspGlyPheValGlnAspIleGlnAsnAspIleHis  
 766 GCCAGTTCTTCCCTGAATGGCAGAAGCACTGAAGAAGTAAAGCCC  
 AlaSerSerSerLeuAsnGlyArgSerThrGluGluValLysPro

Fig. 12

811 ATTGATGAAAACCTTGGGGCAAACCTGGAAAATCTGCTGTTTGCATT  
 IleAspGluAsnLeuGlyGlnThrGlyLysSerAlaValCysIle  
 856 CACCAAGATATAAATGATGATCATGTTGAAGATGTTACAGGAATT  
 HisGlnAspIleAsnAspAspHisValGluAspValThrGlyIle  
 901 CAGCATTTGACAAGCGATTTCAGACAGTGAAGTTTACTGTGATTCT  
 GlnHisLeuThrSerAspSerAspSerGluValTyrCysAspSer  
 946 ATGGAACAATTTGGACAAGAAGAGTCTTTAGACAGCTTTACGTCC  
 MetGluGlnPheGlyGlnGluGluSerLeuAspSerPheThrSer  
 991 AACAAATGGACCATTTCAGTATTACTTGGGTGGTCATTCCAGTCAA  
 AsnAsnGlyProPheGlnTyrTyrLeuGlyGlyHisSerSerGln  
 1036 CCCATGGAAAATTCTGGATTTTCGTGAAGATATTCAAGTACCTCCT  
 ProMetGluAsnSerGlyPheArgGluAspIleGlnValProPro  
 1081 GGAAATGGCAACATTGGGAATATGCAGGTGGTTGCAGTTGAAGGA  
 GlyAsnGlyAsnIleGlyAsnMetGlnValValAlaValGluGly  
 1126 AAAGGTGAAGTCAAGCATGGAGGAGAAGATGGCAGGAATAACAGC  
 LysGlyGluValLysHisGlyGlyGluAspGlyArgAsnAsnSer  
 1171 GGAGCACACACCGGGAGAAGCGAGGCGGAGAACTGACGAATTC  
 GlyAlaProHisArgGluLysArgGlyGlyGluThrAspGluPhe  
 1216 TCTAATGTTAGAAGAGGAAGAGGACATAGGATGCAACACTTGAGC  
 SerAsnValArgArgGlyArgGlyHisArgMetGlnHisLeuSer  
 1261 GAAGGAACCAAGGGCCGGCAGGTGGGAAGTGGAGGTGATGGGGAG  
 GluGlyThrLysGlyArgGlnValGlySerGlyGlyAspGlyGlu  
 1306 CGCTGGGGCTCCGACAGAGGGTCCCGAGGCAGCCTCAATGAGCAG  
 ArgTrpGlySerAspArgGlySerArgGlySerLeuAsnGluGln  
 1351 ATCGCCCTCGTGCTGATGAGACTGCAGGAGGACATGCAGAATGTC  
 IleAlaLeuValLeuMetArgLeuGlnGluAspMetGlnAsnVal  
 1396 CTTTCAGAGACTGCAGAACTGGAAACGCTGACTGCTTTGCAGGCA  
 LeuGlnArgLeuGlnLysLeuGluThrLeuThrAlaLeuGlnAla  
 1441 AAATCATCAACATCAACATTGCAGACTGCTCCTCAGCCCACCTCA  
 LysSerSerThrSerThrLeuGlnThrAlaProGlnProThrSer  
 1486 CAGAGACCATCTTGGTGGCCCTTCGAGATGTCTCCTGGTGTGCTA  
 GlnArgProSerTrpTrpProPheGluMetSerProGlyValLeu  
 1531 ACGTTTGCCATCATATGGCCTTTTATTGCACAGTGGTTGGTGTAT  
 ThrPheAlaIleIleTrpProPheIleAlaGlnTrpLeuValTyr

Fig. 12 Continued

1576 TTATACTATCAAAGAAGGAGAAGAAAAGTGAAGTGAAGGAAAATGG  
LeuTyrTyrGlnArgArgArgArgLysLeuAsn

1621 TGTTCCTCAAGAAGACTACTGGAAGTGGATGACCTCAGAAATGA  
1666 ACTGGATTGTGGTGTTCACAAGAAAATCTTAGTTTGTGATGATTA  
1711 CATTGCTTTTGTGTCCAGTAGTTTAGTTTGTGTACATATATAC  
1756 ACATATATATTTTGCCTACACAAACGATAACATTTTAAGGACTA  
1801 ATATTGCTGATACTTGAATAATCAATCTCTACTAGGTTATAAGTA  
1846 GTATACACAGATTTACCCTGCCCTTGAAGTGAAGGACATTAAAT  
1891 TATTAATGATCATTTGGTAACATGTTTACCTGATTATCTTCCATA  
1936 GAGTAACATAAGCTGCTTTTCAAAGGTACCATTGTGATAATGAGA  
1981 TCAAATTTATAAGTTATTATTTTAAATTTCTAAATTAAATAAAA  
2026 GAAAGAATGCAAAAAAAAAAAAAAAAAAAAAA

Fig. 12 Continued

T020T"050200T

20936375-0-104: 1 ..MYXFHAGSWESWCCCLIPADRPWDRGQHWQLEMADTRSVHETRFEAA 48  
 20936375.0.1: 1 MLFLSFHAGSWESWCCCLIPADRPWDRGQHWQLEMADTRSVHETRFEAA 50

49 VKVIQSLPKNDSFQPTNEMMLKFYSFYKQATEGPCKLSRPGFWDPIGRYK 98  
 51 VKVIQSLPKNGSFQPTNEMMLKFYSFYKQATEGPCKLSRPGFWDPIGRYK 100

99 WDAWSSLGDMTKEEAMIAIYVEEMKKIETMPMTEKVEELLRVIGPFYEIV 148  
 101 WDAWSSLGDMTKEEAMIAIYVEEMKKIETMPMTEKVEELLRVIGPFYEIV 150

149 EDKKSGRSSDITSVRLEKISKCLEDLGNVLTSTPNAKTVNGKAESSDSGA 198  
 151 EDKKSGRSSDITSVRLEKISKCLEDLGNVLTSTPNAKTVNGKAESSDSGA 200

199 ESEEEEEAQEEVKGAEQSDNDKMMKKSADHKNLEIVITNGYDKDGFVQDI 248  
 201 ESEEEEEAQEEVKGAEQSDNDKMMKKSADHKNLEIVITNGYDKDGFVQDI 250

249 QNDIHASSSLNGRSTEEVKPIDENLGQTGKSAVCIHQDINDDHVEDVTGI 298  
 251 QNDIHASSSLNGRSTEEVKPIDENLGQTGKSAVCIHQDINDDHVEDVTGI 300

299 QHLTSDSDSEVYCDSEMFQGEESLDSFTSNNGPFQYYLGGHSSQPMENS 348  
 301 QHLTSDSDSEVYCDSEMFQGEESLDSFTSNNGPFQYYLGGHSSQPMENS 350

349 GFREDIQVPPGNGNIGNMQVVAVEGKGEVKHGGEDGRNNSGAPHREKRG 398  
 351 GFREDIQVPPGNGNIGNMQVVAVEGKGEVKHGGEDGRNNSGAPHREKRG 400

399 ETDEFSNVRGRGRHMQHLSEGTKGRQVSGGDGERWGS DRGSRGSLNEQ 448  
 401 ETDEFSNVRGRGRHMQHLSEGTKGRQVSGGDGERWGS DRGSRGSLNEQ 450

449 IALVLMRLQEDMQNVLQRLQKLETLTALQAKSSTSTLQTAPQPTSQRPSW 498  
 451 IALVLMRLQEDMQNVLQRLQKLEMLTALQAKSSTSTLQTAPQPTSQRPSW 500

499 WPFEMSPGVLTFAIIWPFIAQWL VYLYYQRRRRKLN 534  
 501 WPFEMSPGVLTFAIIWPFIAQWL VYLYYQRRRRKLN 536

Fig. 13

Sequences analyzed:

- 1. 1795045-0-77
- 2. 1795045-0-61

1795045077	MKNQVCSKCGEGYSLGSGEKEDENDEHPAGFSNITATEMDTWAGPSDSRDPGCGNNSSWTFP
1795045061	~~~~~
1795045077	RENVFEENRDDCHVSLTVAVHLKKSGVWFFEXQAVDNNITFEPIQNDQCQEMDITTTDDKW
1795045061	RENVFEENRDDCHVSLTVAVHLKKSGVWFFEXQAVDNNITFEPIQNDQCQEMDITTTDDKW
1795045077	VKLTNDNGEWSHVSNIKSGTNITNWRITGILMGSKAVKPIVMANITTEGVAVITSECFPCK
1795045061	VKLTNDNGEWSHVSNIKSGTNITNWRITGILMGSKAVKPIVMANITTEGVAVITSECFPCK
1795045077	PGITFSNKPGSFNQVCPRNTYSEKGAKECIRCKDDSOFSFEGSSECTERPPCTTKDYFQIT
1795045061	PGITFSNKPGSFNQVCPRNTYSEKGAKECIRCKDDSOFSFEGSSECTERPPCTTKDYFQIT
1795045077	HTPRCDEEGKTOITWKKWIEPKICREDLTDAIRLPPSGEKKDCPPCNPFGYNNGSSSCHPCP
1795045061	HTPRCDEEGKTOITWKKWIEPKICREDLTDAIRLPPSGEKKDCPPCNPFGYNNGSSSCHPCP
1795045077_cura_56	PGITFSDGINKECRRCPAGITEPALGFENKWNVLPGNMKTSCFNVCNSKCDGMNGWEVAGDH
1795045061_cura_54	PGITFSDGINKECRRCPAGITEPALGFENKWNVLPGNMKTSCFNVCNSKCDGMNGWEVAGDH
1795045077_cura_56	IOSCAGGSDNDYITLNLHHPGFKPPTSMTCATGSELGRITFVFETLCSADCVLYFFWVDIN
1795045061_cura_54	IOSCAGGSDNDYITLNLHHPGFKPPTSMTCATGSELGRITFVFETLCSADCVLYFFWVDIN
1795045077_cura_56	RKSTINNVESWGCTTKEKQAYTHITFKNATFTFTWGIPTRELLIOGPR
1795045061_cura_54	RKSTINNVESWGCTTKEKQAYTHITFKNATFTFTWGIPTRELLIOGPR

Fig. 14

Sequences analyzed:

1. 204229740-132-ext-2\_Cura\_56
2. Q64151\_SEMAPHORIN\_4C\_PREC\_Mus
3. Q92854\_SEMAPHORIN
4. 204229742\_Cura\_54
5. 204229740.132\_Cura\_54

204229740132ext2_cura_56	MAPHWA <del>WVIL</del> AAARUWGIGIGAEVMMNIVPRKTVSSGELAVARRRISOTGIODIFLITLITE
204229740132_cura_54	MAPHWA <del>WVIL</del> AAARUWGIGIGAEVMMNIVPRKTVSSGELAVARRRISOTGIODIFLITLITE
204229742_cura_54	MAPHWA <del>WVIL</del> AAARUWGIGIGAEVMMNIVPRKTVSSGELAVARRRISOTGIODIFLITLITE
q64151_semaphorin_4c_prec_mus	MAPHWA <del>WVIL</del> AAARUWGIGIGAEVMMNIVPRKTVSSGELAVARRRISOTGIODIFLITLITE
q92854_semaphorin	MRMCTP <del>RGEL</del> MA <del>L</del> XYMFGTAMAEAPRPIITWEHREYHIV..QHEPDIIVNYSALLISE
204229740132ext2_cura_56	PTGLIIVAGAREALFAR.SMEAT <del>EL</del> IOGATISWEAPVEKKTECTIOKGNNO <del>TE</del> CFNFRFLQP
204229740132_cura_54	PTGLIIVAGAREALFAR.SMEAT <del>EL</del> IOGATISWEAPVEKKTECTIOKGNNO <del>TE</del> CFNFRFLQP
204229742_cura_54	PTGLIIVAGAREALFAR.SMEAT <del>EL</del> IOGATISWEAPVEKKTECTIOKGNNO <del>TE</del> CFNFRFLQP
q64151_semaphorin_4c_prec_mus	PTGLIIVAGAREALFAR.SMEAT <del>EL</del> IOGATISWEAPVEKKTECTIOKGNNO <del>TE</del> CFNFRFLQP
q92854_semaphorin	DKDTL <del>Y</del> TCAREAVAVNA <del>IN</del> ISEKQHEVMKVSE <del>DK</del> AKCA <del>AK</del> CKSKQTEC <del>IN</del> YIRVLQP
204229740132ext2_cura_56	YNASHIVVCGGTVAROPKCHVAVNVIT <del>IT</del> ELTEHGE <del>TE</del> DDKCKCPYDPAKCHAGLIVDGE <del>LI</del> ISA
204229740132_cura_54	YNASHIVVCGGTVAROPKCHVAVNVIT <del>IT</del> ELTEHGE <del>TE</del> DDKCKCPYDPAKCHAGLIVDGE <del>LI</del> ISA
204229742_cura_54	YNASHIVVCGGTVAROPKCHVAVNVIT <del>IT</del> ELTEHGE <del>TE</del> DDKCKCPYDPAKCHAGLIVDGE <del>LI</del> ISA
q64151_semaphorin_4c_prec_mus	YNASHIVVCGGTVAROPKCHVAVNVIT <del>IT</del> ELTEHGE <del>TE</del> DDKCKCPYDPAKCHAGLIVDGE <del>LI</del> ISA
q92854_semaphorin	LSATS <del>IS</del> LVCCGTVAROPACDH <del>IN</del> ITSEKF.LCKN <del>ED</del> CKGRCPEDPAHSYTSVAVDGE <del>LI</del> ISG
204229740132ext2_cura_56	TTANNIT <del>CE</del> TEPPI <del>TE</del> ERNMGP <del>HH</del> SWK <del>TE</del> ELAFEMINERPHVGSAAVPE <del>SV</del> CSF <del>TC</del> GGDDDKVAT <del>TE</del>
204229740132_cura_54	TTANNIT <del>CE</del> TEPPI <del>TE</del> ERNMGP <del>HH</del> SWK <del>TE</del> ELAFEMINERPHVGSAAVPE <del>SV</del> CSF <del>TC</del> GGDDDKVAT <del>TE</del>
204229742_cura_54	TTANNIT <del>CE</del> TEPPI <del>TE</del> ERNMGP <del>HH</del> SWK <del>TE</del> ELAFEMINERPHVGSAAVPE <del>SV</del> CSF <del>TC</del> GGDDDKVAT <del>TE</del>
q64151_semaphorin_4c_prec_mus	TTANNIT <del>CE</del> TEPPI <del>TE</del> ERNMGP <del>HH</del> SWK <del>TE</del> ELAFEMINERPHVGSAAVPE <del>SV</del> CSF <del>TC</del> GGDDDKVAT <del>TE</del>
q92854_semaphorin	TSYNIT <del>CE</del> SEPI <del>TE</del> ISRN.SHSPL <del>AR</del> TEHVAIPMINERSEV <del>FA</del> DVLRKSP <del>DS</del> PDCE <del>ED</del> DKVAT <del>TE</del>
204229740132ext2_cura_56	RERAVESDCVATQWVARVARVCKGDMGCGART <del>TE</del> ORKW <del>IT</del> TEFLKARLAC <del>SA</del> PNWOL <del>IF</del> NQLOA
204229740132_cura_54	RERAVESDCVATQWVARVARVCKGDMGCGART <del>TE</del> ORKW <del>IT</del> TEFLKARLAC <del>SA</del> PNWOL <del>IF</del> NQLOA
204229742_cura_54	RERAVESDCVATQWVARVARVCKGDMGCGART <del>TE</del> ORKW <del>IT</del> TEFLKARLAC <del>SA</del> PNWOL <del>IF</del> NQLOA
q64151_semaphorin_4c_prec_mus	SE <del>RA</del> VE <del>YD</del> CS <del>EO</del> QWVARVARVCKGDMGCGART <del>TE</del> ORKW <del>IT</del> TEFLKARLAC <del>SA</del> PNWOL <del>IF</del> NQLOA
q92854_semaphorin	TEVS <del>ME</del> YEFV <del>FR</del> VZ <del>IP</del> PRVARVCKG <del>QD</del> QGLR <del>IT</del> TEOKK <del>WT</del> SEFLKARLAC <del>SA</del> PNWOL <del>IF</del> NQLOA

Fig. 15A



204229740132ext2_cura_56	~
204229740132_cura_54	~
204229742_cura_54	~
q64151_semaphorin_4c_prec_mus	LPKEPASPFRPGPETDEKLWDVPVGYYSDDGSLKIVPGHARCQPGGGPPSPPPGIPGQPL
q92854_semaphorin	PKIVINTVPQLHSEKTMYLKSSDNRLIMSLFLFFVLFCLFFYNCYKGYLPRQCLKFRS
204229740132ext2_cura_56	~
204229740132_cura_54	~
204229742_cura_54	~
q64151_semaphorin_4c_prec_mus	PSPTRLHLGGGRNSNANGVYVRLQLGGEDRGGSGHPLPELADELRRKLQQRQPLPDSNPEE
q92854_semaphorin	ALLIGKKPKSDFCDREQSLKETLVEPGSFQQNGEHPKPAIDTGYETEQDTITTSKVPTD
204229740132ext2_cura_56	~
204229740132_cura_54	~
204229742_cura_54	~
q64151_semaphorin_4c_prec_mus	SSV~
q92854_semaphorin	REDSQRIDDLsARDKPFVDVKCELKFADSDADGD

Fig. 15C



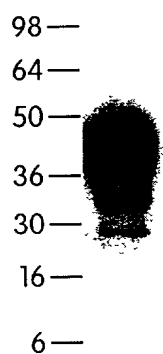


Fig. 16

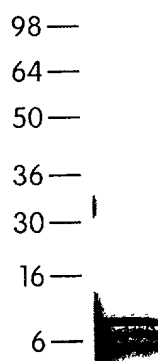


Fig. 17

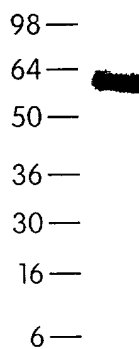


Fig. 18

2025-10-10 10:00:00

Tissue Source	Relative Expression (%)				
	3445452	17089878	1795045.0.61	20422974	20936375.0.104
Endothelial cells	0.00	0.00	1.88	1.11	8.72
Endothelial cells (treated)	0.00	0.01	4.58	1.99	9.74
Pancreas	2.05	0.32	2.68	5.63	16.49
Pancreatic ca. CAPAN 2	0.01	0.00	0.07	1.91	40.05
Adipose	0.24	1.48	6.70	10.01	51.05
Adrenal gland	0.92	0.43	1.36	9.54	75.26
Thyroid	21.17	0.00	1.96	6.25	30.78
Salivary glands	7.59	0.13	1.56	5.67	24.66
Pituitary gland	0.05	0.07	1.11	10.73	10.81
Brain (fetal)	0.17	15.18	3.59	12.41	25.00
Brain (whole)	1.96	34.15	52.85	28.32	38.16
Brain (amygdala)	1.03	19.89	7.13	7.97	46.33
Brain (cerebellum)	4.64	29.73	76.84	29.32	55.86
Brain (hippocampus)	2.98	28.32	27.17	33.45	57.04
Brain (hypothalamus)	10.51	1.18	12.67	4.12	38.69
Brain (substantia nigra)	6.25	7.18	23.49	16.61	67.36
Brain (thalamus)	4.80	6.00	22.53	13.68	69.26
Spinal cord	1.76	4.24	7.64	29.12	50.70
CNS ca. (glio/astro) U87-MG	0.03	0.00	1.99	2.16	29.73
CNS ca. (glio/astro) U-118-MG	0.00	3.54	1.25	2.34	12.33
CNS ca. (astro) SW1783	0.00	0.17	0.00	0.74	13.03
CNS ca.* (neuro.met) SK-N-AS	0.00	0.43	4.30	10.01	93.95
CNS ca. (astro) SF-539	0.07	0.14	0.00	9.81	14.16
CNS ca. (astro) SNB-75	0.00	0.06	0.23	11.58	8.84
CNS ca. (glio) SNB-19	0.01	0.58	0.11	5.15	33.45
CNS ca. (glio) U251	0.01	0.00	0.01	1.58	8.42
CNS ca. (glio) SF-295	0.00	0.00	0.01	3.77	10.44
Heart	33.92	0.01	1.82	7.64	100.00
Skeletal muscle	100.00	0.00	1.00	3.06	79.00
Bone marrow	1.05	3.72	0.43	1.69	18.17
Thymus	0.30	0.21	4.42	6.12	28.52
Spleen	0.14	0.13	2.59	17.43	24.49
Lymph node	0.28	0.28	1.92	10.51	11.74

Fig. 19

SECX	Clone Number	Tissue Expression	Length (nt)	ORF (nt)	Amine Acid Length	Calculate Molecular Weight of Encoded Protein	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
1	3445452	Prostate Gland	932	113-796	227	25734.1	Identities 52/128 (40%); Positives 72/128 (56%) with ACC:P31044 Phosphatidylethanolamine e-Binding Protein (PEBP); 23Kd Morphine Binding Protein (P23K) <i>Rattus norvegicus</i> . 187 amino acid residues.	Identities 44/120 (36%); Positives 66/120 (55%) with ACC:P31044 Phosphatidylethanolamine e-Binding Protein (PEBP) <i>Homo sapiens</i> . 186 Amino Acid residues.	yyyy. Most likely cleavage site between positions 22 and 23: VTG-DE.	Outside - Cert=0.7380. Appears to possess a cleavable N-terminal Signal Sequence.
2	4011999	Not Known	734	66-(?)735	223	24499	Identities 55/76 (72%); Positives 61/76 (80%) with ptnr:SPTRMBL-ACC:Q13670 PMS2-Related Protein HPMSR6 <i>Homo sapiens</i> . 270 amino acid residues.	Identities 48/127 (37%); Positives 69/127 (54%) with ptnr:SPTRMBL-ACC:075631 Uroplakin III <i>Homo sapiens</i> . 287 amino acid residues.	yyyy. Most likely cleavage site between positions 27 and 28: SLS-LD.	Plasma Membrane - Cert.=0.8056. Appears to possess a cleavable N-terminal Signal Sequence.
3	17089878.0.5	Fetal Brain	2762	264-2630	788	88337	Identities 729/788 (92%); Positives 758/788 (96%) with ACC:P79995 Cadherin-10 Precursor <i>Gallus gallus</i> . 789 amino acid residues. Identities 636/650 (97%); Positives 645/650 (99%) with rat cadherin-10. 653 amino acid residues.	Identities 577/790 (73%); Positives 676/790 (85%) with ACC:P55285 Cadherin-6 Precursor (Kidney-Cadherin) <i>Homo sapiens</i> . 790 amino acid residues.	yyyy. Most likely cleavage site between positions 22 and 23:CSECX-EI.	Plasma Membrane - Cert.=0.4600. Appears to possess a cleavable N-terminal Signal Sequence.
4	17089878.0.6	Fetal Brain	1820	285-1704	473	529226	Identities 445/473 (94%); Positives 465/473 (98%) with ACC:P7995 789 aa Cadherin-10 Precursor	Identities 346/476 (72%); Positives 415/476 (87%) with ACC:P55285 human Cadherin-6 precursor Precursor (790 aa)		Plasma Membrane - Cert.=0.7000. Apparently lacks cleavable N-terminal Signal Sequences.

Fig. 20A

SEC No.	Clone Number	Tissue Expression	Nucleotide Length	Open Reading Frame (nt)	Amine Acid Length	Calculate Molecular Weight	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
5	1795045. 0.61	Brain, Thalamus, Pituitary Gland	1508	226-1461	411	46054.5	Identities 511/198 (25%); Positives 711/198 (35%) with ACC:O00276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.	Identities 511/198 (25%); Positives 711/198 (35%) with ACC:O00276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.		Cytoplasm - Cert.=0.4500. Appears to possess no cleavable N-terminal Signal Sequence.
6	20422974 .0.132	Lymphoid Tissue	2155	166-1938	590	66532.5	Identities 497/582 (85%); Positives 536/582 (92%) with ACC:Q64151 Semaphorin I (M-SEMA) FA Factor in Neural Network Development) <i>Mus musculus</i> . 834 amino acid residues.	Identities 247/506 (48%); Positives 330/506 (65%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20 and 21: GIG-AE.	Microbody (Peroxisome) - Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
7	20422974 _2	Lymphoid Tissue	2284	166-1956	596	66969.8	Identities 498/585 (85%); Positives 540/585 (92%) with ACC:Q64151 Semaphorin I (M-SEMA) FA Factor in Neural Network Development) <i>Mus musculus</i> . 834 amino acid residues.	Identities 265/558 (47%); Positives 353/558 (63%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20 and 21: GIG-AE.	Microbody (Peroxisome) - Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
8	20936375 .0.1	Kidney	1930	148-1758	536	60306.7	Identities 453/531 (85%); Positives 482/531 (90%) with ACC:P07106 Bovine DBI-Related Brain Membrane Protein.	Identities 37/91 (40%); Positives 58/91 (63%) with ACC:O75521 DBI-Related Protein <i>Homo sapiens</i> . 364 Amino acid residues.	nnny. Most likely cleavage site between positions 15 and 16:SWC-CC.	Plasma Membrane - Cert.=0.7000. Appears to possess a cleavable N-terminal Signal Sequence.
9	20936785 .0.1	Brain, Fetal Brain	930	123-626	167	18440	Identities 167/167 (100%) with Human Transmembrane Protein HTMPN-46.	Identities 167/167 (100%) with Human Transmembrane Protein HTMPN-46.	nnny. Most likely cleavage site between positions 31 and 32:TPR-LS.	Plasma Membrane - Cert.=64000. Appears to possess an uncleavable N-terminal Signal Sequence. Likely a Type IIIa Membrane Protein

Fig. 20B

SEC No.	Clone Number	Tissue Expression	Nucleotide Length	ORF	Amino Acid Length	Calculated Molecular Weight	Protein Similarity (BLASTP Non-Redundant Composite Database)	Protein Similarity (Human Sequence)	Signal Peptide Cleavage Site (nt)	Cellular Localization
10	1795045. 0.77	Brain, Thalamus	1737	296-1690	464	51645.6	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:000276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.	Identities 51/198 (25%); Positives 71/198 (35%) with ACC:000276 Lymphocyte-Associated Receptor of Death 2 <i>Homo sapiens</i> . 510 amino acid residues.		Cytoplasm- Cert.=0.4500. Appears to possess no cleavable N-terminal Signal Sequence.
11	20422974 0.132_ex t2	Lymphoid Tissue, Aorta, Breast, Colon, Foreskin, Germ Cell, Muscle, Prostate, Spleen, Stomach, and Uterus.	2156	166-2040	624	70478.1	Identities 501/599 (83%); Positives 542/599 (90%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	Identities 501/599 (83%); Positives 542/599 (90%) with ACC:Q92854 Semaphorin <i>Homo sapiens</i> . 862 Amino Acid residues.	yyyy. Most likely cleavage site between positions 20 and 21: GIG-AE.	Microbody (Peroxisome)- Cert.=7480. Appears to possess a cleavable N-terminal Signal Sequence.
12	20936375 0.104	Kidney	1930	7-1611	534	60037.3	Identities 453/531 (85%); Positives 482/531 (90%) with ACC:P07106 Bovine DBI-Related Brain Membrane Protein.	Identities 37/91 (40%); Positives 58/91 (63%) with ACC:O75521 DBI-Related Protein <i>Homo sapiens</i> . 364 amino acid residues.		Plasma Membrane - Cert.=0.7300. Appears not to possess a cleavable N-terminal Signal Sequence.

Fig. 20C